

OM protein - protein search, using sw model

Run on: March 17, 2003, 16:37:52 ; Search time 32 Seconds
(without alignments)
1674.133 Million cell updates/sec

Title: US-09-840-243B-11

Perfect score: 1341

Sequence: MELTQPAEDELIQTTQQTASE.....VIENHILKLFQSNLVPADPE 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1

Q9H9E1 ID Q9H9E1 PRELIMINARY; PRT; 313 AA.

AC Q9H9E1; DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 21, Last annotation update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CDNA FLJ12814 fis, clone NT2RP202520, weakly similar to Homo sapiens transcription factor RFX-B (RFXB) mRNA (Ankyrin) (Ankyrin-repeat family A protein 2) (Hypothetical 34.3 kDa protein).
DE family A protein 2)
GN ANKRA2.
OS Homo sapiens (Human).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Bivalvia; Eutheria; Primates; Cetartiodactyla; Hominidae; Homo. OC NCBI_TaxID=9606;
RN [1] SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H., RA Tanase T., Nomura Y., Togoya S., Komai F., Hara R., Takeuchi K., RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J., RA Wakamatsu A., Nakamura Y., Nagahashi K., Masuho Y., Oshima A.; RA "NEDO human cDNA sequencing project.";
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
RN [2] SEQUENCE FROM N.A.
RA Mao Y., Xie Y., Zhou Z., Zhao W., Zhao S., Wang W., Huang Y., Wang S., RA Tang R., Chen X., Wu C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN [3] SEQUENCE FROM N.A.
RX MEDLINE=20422473; PubMed=10965114;
RA Rader K., Boyer A.D., Farquhar M.G., Arden K.C.;
RT "Assignment of ankyrin repeat, family A (RFXANK-like) 2 (ANKRA2) to human chromosome 5q12->q13 by radiation hybrid mapping and somatic cell hybrid PCR.;"
RT Cytogenet. Cell Genet. 89:164-165 (2000).
RL Cytogenet. Cell Genet. 89:164-165 (2000).
RN [4] SEQUENCE FROM N.A.

Q9uf42 homo sapien
Q9erda rattus norv
Q9cub2 mus musculu
Q96jfl1 homo sapien
Q96f53 homo sapien
Q96kh4 homo sapien
Q9vqil drosophila
Q9czk6 mus musculu
Q96gk0 homo sapien
Q9w2i1 drosophila
Q8wy90 homo sapien
Q8tefl1 homo sapien
Q8wrg7 drosophila
Q9sr03 arabidopsis
Q9ha95 homo sapien
Q9et47 mus musculu
Q9gm49 macaca fasc
Q99407 homo sapien
Q9h6j9 homo sapien
Q9vca7 drosophila
Q96g77 homo sapien
Q14349 homo sapien
Q9uql8 homo sapien

ALIGNMENTS

RA Rader K.A., Orlando R.A., Lou X., Farquhar M.G.; "Characterization of ANKRA, a novel ankyrin repeat protein that interacts with the cytoplasmic domain of megalin.", J. Am. Soc. Nephrol. 11:0-0 (2001). [5]

RT TISSUE=KIDNEY;

RL Strausberg R.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

RC EMBL; AF314032; AAK01621.1; -;

RA EMBL; AK022876; BAB14288.1; -;

RL EMBL; AF251051; AAK34941.1; -;

RC EMBL; AF314032; AAK01621.1; -;

RA EMBL; BC012917; AAH12917.1; -;

RL HSSP; P80144; 2MYO.

RC InterPro; IPR002110; ANK.

RA Pfam; PF00023; ank; 3.

RC PRINTS; PR01415; ANKYRIN.

RA SMART; SM00248; ANK; 3.

RA PROSITE; PS50088; ANK_REPEAT; 3.

RA PROSITE; PS50297; ANK REP REGION; 1.

RC ANK repeat; Hypothetical protein; Repeat.

RA SEQUENCE; 313 AA; 34272 MW; 3B52B1415B7A5AFA CRC64;

Query Match Best Local Similarity 46.3%; Score 621.5; DB 4; Length 313; Matches 126; Conservative 26; Mismatches 49; Indels 7; Gaps 2;

QY 51 NPEPDASV-----SSPQAGSSLKHSTTLNQRGNEVSALPATLDSLTIHQLAQGELD 104

Db 104 SPSPGIQVRHVYTPSTKHFSPPIKQSTTLNKHRCNEVSTPLANSLSAHQLAQGELM 162

QY 105 QLKEHLRKGDNLVNKPDERGFTPLIWAASFGEIETVRLFLEWGADPHILAKERESALSLA 164

Db 164 YLATRIEQ-ENVINHTDEEGFTPLMWAAGHQIAVVEFLONGADPOLLGKGRRESALSLA 222

QY 165 STGGYTDIVGLLERDWDINIYDWNNGGTPLLYAVRGNHVKCVEALLARGADLTTEADSGY 224

Db 223 CSKGYTDIVKMLLDCCGVDVNEYDWNGGTPLLYAVHGNHVKCVKMLLESGADPTIETDSY 282

QY 225 TPMDLAVALGYRKVQQVIEHILKLQFOS 252

Db 283 NSMDLAVALGYRSVQQVIESHLKLQN 310

RESULT 2

Q99PE2 ID Q99PE2 PRELIMINARY; PRT; 312 AA.

AC Q99PE2; 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Ankyrin-repeat family A protein.

GN ANKRA2 OR 1110004M18R1K.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. [1]

RN NCBI_TaxID=10090; OX NCBI_TaxID=10090; RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN= C57BL/6J; TISSUE= EMBRYO; MEDLINE= 21085660; PubMed= 11217851;

RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Cytogenet. Cell Genet. 89:164-165 (2000). [2]

RN SEQUENCE FROM N.A. MEDLINE= 20422473; PubMed= 10965114;

RX Rader K., Boyer A.D., Farquhar M.G., Arden K.C.; "Assignment of ankyrin repeat, family A (RFXANK-like) 2 (ANKRA2) to human chromosome 5q12->q13 by radiation hybrid mapping and somatic cell hybrid PCR.", Cytogenet. Cell Genet. 89:164-165 (2000). [2]

RN SEQUENCE FROM N.A. MEDLINE= 20547411; PubMed= 11095640;

RX Rader K., Orlando R.A., Lou X., Farquhar M.G.; "Characterization of ANKRA, a novel ankyrin repeat protein that interacts with the cytoplasmic domain of megalin.", J. Am. Soc. Nephrol. 11:2167-2178 (2000). [3]

RT EMBL; AF314031; AAK01620.1; -;

DR HSSP; P80144; 2MYO.

DR InterPro; IPR002110; ANK.

DR Pfam; PF00023; ank; 3.

DR PRINTS; PR01415; ANKYRIN.

DR SMART; SM00248; ANK; 3.

DR PROSITE; PS50088; ANK_REPEAT; 3.

DR PROSITE; PS50297; ANK REP REGION; 1.

DR ANK repeat; Repeat.

DR SEQUENCE; 312 AA; 34062 MW; 3B52B1415B7A5AFA CRC64;

Query Match Best Local Similarity 45.7%; Score 612.5; DB 11; Length 312; Matches 125; Conservative 25; Mismatches 51; Indels 7; Gaps 2;

QY 51 NPEPDASV-----SSPQAGSSLKHSTTLNQRGNEVSALPATLDSLTIHQLAQGELD 104

Db 103 SPSPGIQVRHVYTPSTKHFSPPIKQSTTLNKHRCNEVSTPLANSLSAHQLAQGELM 162

QY 105 QLKEHLRKGDNLVNKPDERGFTPLIWAASFGEIETVRLFLEWGADPHILAKERESALSLA 164

Db 163 YLATRIEQ-ENVINHTDEEGFTPLMWAAGHQIAVVEFLONGADPOLLGKGRRESALSLA 221

QY 165 STGGYTDIVGLLERDWDINIYDWNNGGTPLLYAVRGNHVKCVEALLARGADLTTEADSGY 224

Db 222 CSKGYTDIVKMLLDCCGVDVNEYDWNGGTPLLYAVHGNHVKCVKMLLESGADPTIETDSY 281

QY 225 TPMDLAVALGYRKVQQVIEHILKLQFOS 252

Db 282 NSMDLAVALGYRSVQQVIESHLKLQN 309

RESULT 3

Q9D1J8 ID Q9D1J8 PRELIMINARY; PRT; 154 AA.

AC Q9D1J8; 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 21, Last annotation update)

DE 1110004M18R1K protein.

GN ANKRA2 OR 1110004M18R1K.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. [1]

RN NCBI_TaxID=10090; OX NCBI_TaxID=10090; RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN= C57BL/6J; TISSUE= EMBRYO; MEDLINE= 21085660; PubMed= 11217851;

RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Cytogenet. Cell Genet. 89:164-165 (2000). [2]

RN SEQUENCE FROM N.A. MEDLINE= 20422473; PubMed= 10965114;

RX Rader K., Boyer A.D., Farquhar M.G., Arden K.C.; "Assignment of ankyrin repeat, family A (RFXANK-like) 2 (ANKRA2) to human chromosome 5q12->q13 by radiation hybrid mapping and somatic cell hybrid PCR.", Cytogenet. Cell Genet. 89:164-165 (2000). [2]

RN SEQUENCE FROM N.A. MEDLINE= 20547411; PubMed= 11095640;

RX Rader K., Orlando R.A., Lou X., Farquhar M.G.; "Characterization of ANKRA, a novel ankyrin repeat protein that interacts with the cytoplasmic domain of megalin.", J. Am. Soc. Nephrol. 11:2167-2178 (2000). [3]

RT EMBL; AF314031; AAK01620.1; -;

DR HSSP; P80144; 2MYO.

DR MGII:1915808; Ankras2.

DR InterPro; IPR002110; ANK.

Query Match 32.7%; Score 439; DB 11; Length 154;
 Best Local Similarity 68.3%; Pred. No. 2.4e-29;
 Matches 84; Conservative 13; Mismatches 26; Indels 0; Gaps 0;
 RIL RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Liao P., Liao G., Miranda A., Mungall C.J.,
 RA Nuno J., Pacleb J., Paragas V., Park S., Mirouanenavong S., Wan K.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Celniker S.,
 RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AE003626; AAF52838.2; -.
 DR EMBL; AY061547; AAL29095.1; -.
 DR HSSP; P80144; 2MYS.
 DR FlyBase; FBgn0032171; CG5846.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; ank; 4.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 3.
 DR PROSITE; PS50088; ANK_REPEAT; 2.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 KW ANK repeat; Repeat.
 SQ SEQUENCE 234 AA; 2483.8 MW; A4E8DFBF97BF0514 CRC64;

Query Match 20.4%; Score 274; DB 5; Length 234;
 Best Local Similarity 33.8%; Pred. No. 3.6e-15;
 Matches 80; Conservative 37; Mismatches 96; Indels 24; Gaps 6;
 RIL RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtt K.C., Busam D.A., Butler H., Cadieu E., Chandra I.,
 RA Cherry J.M., Cawley S., Dahake C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin R.K.J., Evangelista C.C., Ferrera S., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Query Match 17.4%; Score 439; DB 11; Length 154;
 Best Local Similarity 68.3%; Pred. No. 2.4e-29;
 Matches 84; Conservative 13; Mismatches 26; Indels 0; Gaps 0;
 RIL RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
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 RA Gibbs R.A., Myers E.W., Rubin G.M., Celniker S.,
 RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AE003626; AAF52838.2; -.
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 DR HSSP; P80144; 2MYS.
 DR FlyBase; FBgn0032171; CG5846.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; ank; 4.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 3.
 DR PROSITE; PS50088; ANK_REPEAT; 2.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 KW ANK repeat; Repeat.
 SQ SEQUENCE 234 AA; 2483.8 MW; A4E8DFBF97BF0514 CRC64;

Query Match 13.0%; Score 274; DB 5; Length 234;
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 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
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 RA Durbin R.K.J., Evangelista C.C., Ferrera S., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
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 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
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 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
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 RA Cherry J.M., Cawley S., Dahake C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin R.K.J., Evangelista C.C., Ferrera S., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Query Match 13.0%; Score 274; DB 5; Length 234;
 Best Local Similarity 33.8%; Pred. No. 3.6e-15;
 Matches 80; Conservative 37; Mismatches 96; Indels 24; Gaps 6;
 RIL RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtt K.C., Busam D.A., Butler H., Cadieu E., Chandra I.,
 RA Cherry J.M., Cawley S., Dahake C., Davenport L.B., Davies P.,
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 RA Durbin R.K.J., Evangelista C.C., Ferrera S., Ferreira S., Fleischmann W.,
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 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
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 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

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 Best Local Similarity 33.8%; Pred. No. 3.6e-15;
 Matches 80; Conservative 37; Mismatches 96; Indels 24; Gaps 6;
 RIL RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
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 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtt K.C., Busam D.A., Butler H., Cadieu E., Chandra I.,
 RA Cherry J.M., Cawley S., Dahake C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
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 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
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 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
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 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

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 RIL RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA MEDLINE=20196006; PubMed=10731132;
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 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue

RL	DNA Res. 8:205-213 (2001).	SQ	SEQUENCE	1786 AA;	195550 MW;	03E220FB521747F1 CRC64;
DR	EMBL; AP003590; BAB74447.1; -.					
DR	InterPro; IPR02110; ANK.					
DR	Pfam; PF00023; ank; 13.					
DR	PRINTS; PR01415; ANKYRIN.					
DR	SMART; SM00248; ANK; 13.					
DR	PROSITE; PS50088; ANK_REPEAT; 11.					
KW	Hypothetical protein; Complete proteome.					
SQ	SEQUENCE 426 AA; 43800 MW; CF0B9E5D43ACAA03 CRC64;					
Query Match	16.4%; Score 219.5; DB 16; Length 426;					
Best Local Similarity	30.7%; Pred. No. 3.5e-10;					
Matches	62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;					
Matches	62; Conservative 34; Mismatches 71; Indels 35; Gaps 4;					
QY	62 QAGSSLKHSTTL-----TNRQNGNEVSALPATIDSLSIHQLAAQGELDOLK 107	QY	19 SELGDPEDPGEAADGSDTIVVLSLFPCTPEPVNPEPDASVSSPQAGSSLKHSTTLNRQR 78			
Db	234 QDGE SALHLATVEGYVVDVQVLLNQGANTQIKNKLGDTPLLVAALQH-----DQIV 285	Db	2 SNEGDPQQQQPESQEVOA---PAAPEPGRAE----- 32			
QY	108 EHLRK-----GDNLVNKPDERGFPLI WASAFEIETVRFLEWGA DPHLAKERESAL 161	QY	79 GNEVSALPATIDSLSIHQLAAQGELDOLKEHLRKGDNLVNKPDERGFPLI WASAFEIETVRFLEWGA DPHLAKERESAL 138			
Db	286 ETLKYGANVHGDNL-----GETPLT LAASQGHTATVRILLDYGANANAPIASDGKTA L 338	Db	33 -----GSASFLRAAGDLEKVL ELLRAGTD-INTSNANGLNSLHLASKEGHSE 80			
QY	162 SLASTGGYTDIVGLL ERDVDIN YDWNGGTPPLIYAVRGHNVKCV EALLARGADLTTEAD 221	QY	139 TWRFLLEWGA DPHLAKERESAL SLASTGGYTDIVGLL ERDVDIN YDWNGGTPPLIYAV 198			
Db	339 IKATERNHPGV IQQLLA KGANVNVQDSV GAT ALIWAASGGY GYNK WQI LLEGGA DTN LKNR 398	Db	81 VVRELIK RQAOVDAATRKGN TALHIA SLAGOSLIVT L VENGANVNVQSVNGF TPLYMA 140			
QY	222 SGYTPMDL AVALG YR KVQVIE 243	QY	199 RGNHVKCV EALLARGADLTTEADSGYTPMDL AVALG YR KVQVIE 244			
Db	399 GGYT ALMIA EFNG FRSIV QILK 420	Db	141 QENHEEVV KYLLKH GANQAL STEDGFTPLAVALQ QGHDRVVAVLLEN 187			
RESULT 6		RESULT 7				
ID	Q17344 PRELIMINARY; PRT; 1786 AA.	ID	Q17487 PRELIMINARY; PRT; 1809 AA.			
AC	Q17344;	AC	Q17487;			
DT	01-NOV-1996 (TREMBIrel. 01, Created)	DT	01-NOV-1996 (TREMBIrel. 01, Last sequence update)			
DT	01-MAR-2002 (TREMBIrel. 20, Last annotation update)	DT	01-NOV-1996 (TREMBIrel. 01, Last sequence update)			
DE	UNC-44 (Fragment).	DE	01-MAR-2002 (TREMBIrel. 20, Last annotation update)			
GN		DE	E. elegans ankyrin-related unc-44 (GB:U21734).			
OS		GN	UNC-44.			
OS	Caenorhabditis elegans.	OS				
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;	OC				
OC	Rhabditidae; Peloderinae; Caenorhabditis.	OC				
OX	NCBI_TaxID=6239;	OX				
RP	SEQUENCE FROM N.A.	RP				
RX	MEDLINE=94150718; PubMed=7906398;	RX				
RA	Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,	RA				
RA	Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,	RA				
RA	Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,	RA				
RA	Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,	RA				
RA	Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,	RA				
RA	Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,	RA				
RA	Parsons J., Percy C., Rifkin L., Roopa A., Saunders D., Shownkeen R.,	RA				
RA	Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,	RA				
RA	Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,	RA				
RA	Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,	RA				
RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";	RT				
RL	RT elegans.";	RL				
RL	RT Nature 368:32-38 (1994).	RL				
RN	RT [2]	RN				
RP	SEQUENCE FROM N.A.	RP				
RA	RT Gattung S.;	RA				
RT	RT "The sequence of C. elegans cosmid B0350.";	RT				
RL	RT Submitted (MAR-1996) to the EMBL/GenBank/DDJB databases.	RL				
RN	RT [3]	RN				
RP	SEQUENCE FROM N.A.	RP				
RA	Waterston R.;	RA				
RA	Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.	RA				
DR	EMBL; U50071; AAA93446.1; -.	DR				
DR	HSSP; P42773; 1IHB.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.	DR				
DR	InterPro; IPR00488; Death.	DR				
DR	InterPro; IPR000906; ZU5.	DR				
DR	InterPro; IPR002110; ANK.					

Query Match 16.0%; Score 214; DB 5; Length 1809;
 Best Local Similarity 27.3%; Pred. No. 8.9e-09; Mismatches 87; Indels 42; Gaps 4;
 Matches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;
 RC STRAIN=N2;
 RA Otsuka A.J.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A..

QY 19 SELGDPEDPGEAAADGSDTIVVLSPCTPEPVNPEDASVSSPQAGSSLKHSTTLNRQR 78
 DB 2 SNEGDPQPQQQQPESQEVQA---PAAPEPGRAE----- 32

QY 79 GNEVSALPATLDSLSIHQLAAQGELDQKLKEHLRKGDNLVNPDPERGFTPLIWAQAFGEIE 138
 DB 33 -----GSASFLRAARAGDLEKVLLELRAGTD-INTSNANGLNSLHLASKEGHSE 80

QY 139 TVERFLLEWGADPHILAKERESALSLASTGGYTDIVGLLERDWDINYYDWNGGTPLLYAV 198
 DB 81 VVERELIKRQAQDAATRKGNNTALHIAASLAGOSLIVLIVENGANVNVQSVNGFTPLYMA 140

QY 199 RGNHVKCVAELLARGADLTTEADSGYTPMDLAVALGY-RKVQVQIEN 244
 DB 141 QENHEEVVKYLLKHGANQALSTEDGFTPLAVALQQGHDRVAVLEN 187

RESULT 8

ID Q17488 PRELIMINARY; PRT; 1815 AA.
 AC 017488; 002517;
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE C. ELEGANS ankyrin-related, UNC-44 (GB:U21734).

GN NCBI_TaxID=6239;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderrinae; Caenorhabditis.

RN [1] SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
 RA Smalton N., Smith A., Sonnhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans. "; Nature 368:32-38 (1994).
 RN [2] SEQUENCE FROM N.A.
 RP Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
 RN [3] SEQUENCE FROM N.A.
 RP Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
 RN [4] SEQUENCE FROM N.A.
 RC STRAIN=N2;
 RX MEDLINE=95263663; PubMed=7744957;
 RA Otsuka A.J., Franco R., Yang B., Shim K., Tang L.Z., Zhang Y.,
 RA Boontrakulpoontawee P., Jeyaprakash A., Hedgecock E., Wheaton V.I.,
 RA Sobery A.;

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 RP SEQUENCE FROM N.A..

QY 19 SELGDPEDPGEAAADGSDTIVVLSPCTPEPVNPEDASVSSPQAGSSLKHSTTLNRQR 78
 DB 2 SNEGDPQPQQQQPESQEVQA---PAAPEPGRAE----- 32

QY 79 GNEVSALPATLDSLSIHQLAAQGELDQKLKEHLRKGDNLVNPDPERGFTPLIWAQAFGEIE 138
 DB 33 -----GSASFLRAARAGDLEKVLLELRAGTD-INTSNANGLNSLHLASKEGHSE 80

QY 139 TVERFLLEWGADPHILAKERESALSLASTGGYTDIVGLLERDWDINYYDWNGGTPLLYAV 198
 DB 81 VVERELIKRQAQDAATRKGNNTALHIAASLAGOSLIVLIVENGANVNVQSVNGFTPLYMA 140

QY 199 RGNHVKCVAELLARGADLTTEADSGYTPMDLAVALGY-RKVQVQIEN 244
 DB 141 QENHEEVVKYLLKHGANQALSTEDGFTPLAVALQQGHDRVAVLEN 187

RESULT 9

ID Q17486 PRELIMINARY; PRT; 1867 AA.
 AC 017486; 002516;
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE C. ELEGANS ankyrin-related, UNC-44.

GN NCBI_TaxID=6239;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderrinae; Caenorhabditis.

RN [1] SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

QY	19	SELGDPEDPGEAAADGSDTIVVLSLFPCTPEPVNPEDASVSSPQAGSSLKHSTTLNRQR	78	RA Craxton M., Dear S., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Smaardon N., Smith A., Sonhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P., "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans."; Nature 368:32-38 (1994).	Db	81	VRRELIKRQAOQDAATRKGNNTALHIASLAGQSLIVTILVENGANVNQSVNGFTPLYMAA	140
QY	199	RGNHVKCVEALLARGADLTTEADSGYTPMDLAVALGY-RKVQQTEN	244	RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Smaardon N., Smith A., Sonhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P., "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans."; Nature 368:32-38 (1994).	Qy	199	RGNHVKCVEALLARGADLTTEADSGYTPMDLAVALGY-RKVQQTEN	244
Db	141	QENHEEVVKILKHGANQALSTEDGFTPLAVALQOQGHDRVAVLLEN	187	RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Smaardon N., Smith A., Sonhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P., "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans."; Nature 368:32-38 (1994).	Db	141	QENHEEVVKILKHGANQALSTEDGFTPLAVALQOQGHDRVAVLLEN	187
RT	Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.			RESULT 10				
RL	SEQUENCE FROM N.A.			Q17489				
RP	SEQUENCE FROM N.A.			Q17489	PRELIMINARY;	PRT;	2039	AA.
RA	Gattung S.;			Q17489;				
RA	Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.			01-NOV-1996	(TREMBLrel. 01, Created)			
RL	[3]			01-NOV-1996	(TREMBLrel. 01, Last sequence update)			
RN	SEQUENCE FROM N.A.			01-JUN-2002	(TREMBLrel. 21, Last annotation update)			
RA	Waterson R.;			DE	C. elegans ankyrin-related unc-44 (GB:U21734).			
RL	Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.			GN	UNC-44.			
RP	SEQUENCE FROM N.A.			OS	Caenorhabditis elegans.			
RA	STRAIN=N2;			OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;			
RC				NCBI_TaxID=6239;				
RX	MEDLINE=95263663; PubMed=7744957;			RN				
RA	Otsuka A.J., Franco R., Yang B., Shim K., Tang L.Z., Zhang Y.,			RP	SEQUENCE FROM N.A.			
RA	Boontrakulpoontawee P., Jeyaprakash A., Hedgecock E., Wheaton V.I.,			RX	MEDLINE=94150718; PubMed=7906398;			
RA	Sobery A.;			RA	Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,			
RT	"An ankyrin-related gene (unc-44) is necessary for proper axonal			RA	Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,			
RT	guidance in <i>Caenorhabditis elegans</i> ."; J. Cell Biol. 129:1081-1092 (1995).			RA	Craxton M., Dear S., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Smaardon N., Smith A., Sonhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P., "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans."; Nature 368:32-38 (1994).			
RL	SEQUENCE FROM N.A.			RA	Strain=N2;			
RC	SEQUENCE FROM N.A.			RA	Otsuka A.J.;			
RA	Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.			RA	Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.			
RL	[16]			RA	Otsuka A.J.;			
RP	SEQUENCE FROM N.A.			RA	Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.			
RC	SEQUENCE FROM N.A.			RA	Strain=N2;			
RA	Otsuka A.J.;			RA	Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.			
RL	Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.			RA	EMBL; U50071; AAA93444.1; -.			
DR	EMBL; U50071; AAA93444.1; -.			RA	EMBL; U50071; AAA93444.1; -.			
DR	HSSP; U39847; AAB41828.1; -.			RA	EMBL; U50071; AAA93444.1; -.			
DR	HSSP; P42773; 1IHB.			RA	EMBL; U50071; AAA93444.1; -.			
DR	InterPro; IPR002110; ANK.			RA	EMBL; U50071; AAA93444.1; -.			
DR	InterPro; IPR000488; Death.			RA	EMBL; U50071; AAA93444.1; -.			
DR	InterPro; IPR001360; GH 1.			RA	EMBL; U50071; AAA93444.1; -.			
DR	InterPro; IPR000906; ZU5.			RA	EMBL; U50071; AAA93444.1; -.			
DR	Pfam; PF00023; ank; 24.			RA	EMBL; U50071; AAA93444.1; -.			
DR	Pfam; PF00531; death; 1.			RA	EMBL; U50071; AAA93444.1; -.			
DR	Pfam; PF00791; ZU5; 1.			RA	EMBL; U50071; AAA93444.1; -.			
DR	PRINTS; PR01415; ANKYRIN.			RA	EMBL; U50071; AAA93444.1; -.			
DR	SMART; SM00248; ANK; 21.			RA	EMBL; U50071; AAA93444.1; -.			
DR	SMART; SM00005; DEATH; 1.			RA	EMBL; U50071; AAA93444.1; -.			
DR	SMART; SM00218; ZU5; 1.			RA	EMBL; U50071; AAA93444.1; -.			
DR	PROSITE; PS50088; ANK_REPEAT; 22.			RA	EMBL; U50071; AAA93444.1; -.			
DR	PROSITE; PS50297; ANK_REPEAT_REGION; 1.			RA	EMBL; U50071; AAA93444.1; -.			
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.			RA	EMBL; U50071; AAA93444.1; -.			
DR	PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_2.			RA	EMBL; U50071; AAA93444.1; -.			
KW	ANK repeat; Repeat.			RA	EMBL; U50071; AAA93444.1; -.			
SQ	SEQUENCE 1867 AA; 204253 MW; 4689A2104623B4C6 CRC64;			RA	EMBL; U50071; AAA93444.1; -.			
Query Match	Best Local Similarity 16.0%; Score 214; DB 5; Length 1867;			RA	EMBL; U50071; AAA93444.1; -.			
Matches	62; Conservative 27.3%; Pred. No. 9.3e-09; Mismatches 87; Indels 42; Gaps 4;			RA	EMBL; U50071; AAA93444.1; -.			
QY	19 SELGDPEDPGEAAADGSDTIVVLSLFPCTPEPVNPEDASVSSPQAGSSLKHSTTLNRQR	78	SEQUENCE FROM N.A.	RT	Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.			
Db	2 SNEGDPQQQQPESQEVQA-PAAPEPGR	32	SEQUENCE FROM N.A.	RL	Waterson R.;			
QY	79 GNEVALPATLDSLTHQLAAQGELDOLKEHLRKGDNLVNKPPDERGFTPLI	138	SEQUENCE FROM N.A.	RP	Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.			
Db	33 -----GSASFLRAAARGDLEKVELLRLRAGTD-INTSNANGLNSLHLASKEGHSE	80	SEQUENCE FROM N.A.	RA	Waterson R.;			
QY	19 SELGDPEDPGEAAADGSDTIVVLSLFPCTPEPVNPEDASVSSPQAGSSLKHSTTLNRQR	78	SEQUENCE FROM N.A.	RA	Waterson R.;			
QY	19 SELGDPEDPGEAAADGSDTIVVLSLFPCTPEPVNPEDASVSSPQAGSSLKHSTTLNRQR	2039	SEQUENCE FROM N.A.	RA	Waterson R.;			
QY	19 SELGDPEDPGEAAADGSDTIVVLSLFPCTPEPVNPEDASVSSPQAGSSLKHSTTLNRQR	7722C4C2E6AFD68A CRC64;	SEQUENCE FROM N.A.	RA	Waterson R.;			
QY	19 SELGDPEDPGEAAADGSDTIVVLSLFPCTPEPVNPEDASVSSPQAGSSLKHSTTLNRQR	7722C4C2E6AFD68A CRC64;	SEQUENCE FROM N.A.	RA	Waterson R.;			

Db	2	SNEGDPPQQQQPESQEVA---PAAPEPGRAE-----	32	QY	79	GNEVSLPATLDSLSIHQLAQGELDQLKEHLRKGDNLVNKPDERGFPTPLIWA	138	QY	79	GNEVSLPATLDSLSIHQLAQGELDQLKEHLRKGDNLVNKPDERGFPTPLIWA	138
QY	79	GNEVSLPATLDSLSIHQLAQGELDQLKEHLRKGDNLVNKPDERGFPTPLIWA	138	QY	79	GNEVSLPATLDSLSIHQLAQGELDQLKEHLRKGDNLVNKPDERGFPTPLIWA	138	QY	79	GNEVSLPATLDSLSIHQLAQGELDQLKEHLRKGDNLVNKPDERGFPTPLIWA	138
Db	33	-----GSASFLLRAARAGDIEKVELLRLAGTD-INTSNANGLNSLHLASKEGHSE	80	Db	33	-----GSASFLLRAARAGDIEKVELLRLAGTD-INTSNANGLNSLHLASKEGHSE	80	Db	33	-----GSASFLLRAARAGDIEKVELLRLAGTD-INTSNANGLNSLHLASKEGHSE	80
Db	81	TVRELIKRQAQVDAATRKGNNTALHIAASLAGQSLIVTILVENGANVNQSVNGFTPLYMAA	140	QY	139	TVRELIKRQAQVDAATRKGNNTALHIAASLAGQSLIVTILVENGANVNQSVNGFTPLYMAA	140	QY	139	TVRELIKRQAQVDAATRKGNNTALHIAASLAGQSLIVTILVENGANVNQSVNGFTPLYMAA	198
Db	141	QENHEEVVKYLLKHGANQALSTEDGFTPLAVALQOQGHDRVAVLEN	187	QY	199	RGNHVVCVEALLARGADLITEADSGYTPMDLAVALGY-RKVQQVIE	244	QY	199	RGNHVVCVEALLARGADLITEADSGYTPMDLAVALGY-RKVQQVIE	244
Db	141	QENHEEVVKYLLKHGANQALSTEDGFTPLAVALQOQGHDRVAVLEN	187	Db	141	QENHEEVVKYLLKHGANQALSTEDGFTPLAVALQOQGHDRVAVLEN	187	Db	141	QENHEEVVKYLLKHGANQALSTEDGFTPLAVALQOQGHDRVAVLEN	187
RESULT 11				RESULT 12				RESULT 12			
Q17343				Q9EQG6				Q9EQG6			
ID	Q17343	PRELIMINARY;	PRT; 6994 AA.	ID	Q9EQG6	PRELIMINARY;	PRT; 1762 AA.	ID	Q9EQG6	PRELIMINARY;	PRT; 1762 AA.
AC	Q17343;			AC	Q9EQG6;			AC	Q9EQG6;		
DT	01-NOV-1996 (TREMBLrel. 01, Created)			DT	01-MAR-2001 (TREMBLrel. 16, Created)			DT	01-OCT-2001 (TREMBLrel. 18, Last sequence update)		
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)			DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			DE	KIDINS220.			DE	KIDINS220.		
DE	UNC-44 ankyrins.			GN	Rattus norvegicus (Rat).			GN	Rattus norvegicus (Rat).		
GN	Caenorhabditis elegans.			OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OS	Bukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.			OC	NCBI_TaxID=10116;			OC	NCBI_TaxID=10116;		
OC				OX				OX			
OX				RN				RN			
RN	SEQUENCE FROM N.A.			RX	SEQUENCE FROM N.A.			RX	SEQUENCE FROM N.A.		
RP				RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
RC	STRAIN=N2;			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
RX	MEDLINE=95263663; PubMed=7744957;			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
RA	Otsuka A.J., Franco R., Yang B., Shim K., Tang L.Z., Zhang Y.,			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
RA	Boontrakulpoontawee P., Jeyaprakash A., Hedgecock E., Wheaton V.I.,			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
RA	Sobey A.;	"An ankyrin-related gene (unc-44) is necessary for proper axonal		RT	"Identification and cloning of Kidins220, a novel neuronal substrate of protein kinase D."			RT	"Identification and cloning of Kidins220, a novel neuronal substrate of protein kinase D."		
RT	guidance in Caenorhabditis elegans.";			RT	J. Biol. Chem. 275:40048-40056 (2000).			RT	J. Biol. Chem. 275:40048-40056 (2000).		
RT	J. Cell Biol. 129:1081-1092 (1995).			RL				RL			
RL	[2]			RN	SEQUENCE FROM N.A.			RN	SEQUENCE FROM N.A.		
RN	REVISIONS, AND SEQUENCE OF 6126-6994 FROM N.A.			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
RP				RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
RC	STRAIN=N2;			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
RA	Otsuka A.J.;	Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.		RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
RA	Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
RL				RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
DR	EMBL; U39847; AAB41827.1; -.			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
DR	EMBL; U21733; AAB38384.1; -.			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
DR	HSSP; P42773; I1HB.			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
DR	InterPro; IPR002110; ANK.			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
DR	InterPro; IPR000488; Death.			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
DR	InterPro; IPR001360; GH ¹ .			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
DR	InterPro; IPR002383; GLA_blood.			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
DR	InterPro; IPR000906; ZU5.			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
DR	Pfam; PF00023; ank; 24.			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
DR	Pfam; PF00531; death; 1.			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
DR	PRINTS; PR01415; ANKYRIN.			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
DR	PRINTS; PR00001; GLABLOOD.			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
DR	SMART; SM00248; ANK; 21.			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
DR	SMART; SM00005; DEATH; 1.			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
DR	SMART; SM00218; ZU5; 1.			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
DR	PROSITE; PS50088; ANK_REPEAT; 22.			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
DR	PROSITE; PS50297; ANK_REPEAT_REGION; 1.			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
DR	PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_2.			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
KW	ANK repeat; Repeat.			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
SQ	SEQUENCE 6994 AA; 775364 MW; 90CB449925D9923D CRC64;			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
Query Match	16.0%; Score 214; DB 5; Length 6994;			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
Best Local Similarity	27.3%; Pred. No. 6.8e-08;			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
Matches	62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;			RA	SEQUENCE FROM N.A.			RA	SEQUENCE FROM N.A.		
QY	19 SELGDPEPDGEEAADGSDTVLISLFPCTPEVNPEPDASVSSPQAGSSLKHSTTLNRQR	78		QY	100 QGELDQKELRKGDNLVNKPDERGFPTPLIWA	159		QY	100 QGELDQKELRKGDNLVNKPDERGFPTPLIWA	159	
Db	2 SNEGDPQQQQPESQEVA---PAAPEPGRAE-----	32		Db	81 EGHIIHVEELLKSGASLEHR-DMGWHTALMWACYKGR	139		Db	81 EGHIIHVEELLKSGASLEHR-DMGWHTALMWACYKGR	139	
QY	2 SNEGDPQQQQPESQEVA---PAAPEPGRAE-----	32		QY	160 ALSLASTGGYTDIVGLLERDWDINTYDWNGGTPLLYAV	219		QY	160 ALSLASTGGYTDIVGLLERDWDINTYDWNGGTPLLYAV	219	
Db	81 TVRELIKRQAQVDAATRKGNNTALHIAASLAGQSLIVTILVENGANVNQSVNGFTPLYMAA	140		Db	140 PIWAAGRHHADIVHILLQNGAKVNCSDKYGTTPLW	199		Db	140 PIWAAGRHHADIVHILLQNGAKVNCSDKYGTTPLW	199	
QY	199 RGNHVVCVEALLARGADLITEADSGYTPMDLAVALGY-RKVQQVIE	244		QY	220 ADSGYTPMDLAVALGY-RKVQQVIE	245		QY	220 ADSGYTPMDLAVALGY-RKVQQVIE	245	
Db	141 QENHEEVVKYLLKHGANQALSTEDGFTPLAVALQOQGHDRVAVLEN	187		Db	200 GANSMTALIVAVKGGYTQSVEILKRN	226		Db	200 GANSMTALIVAVKGGYTQSVEILKRN	226	
RESULT 13				RESULT 13				RESULT 13			
Q9ULH0				Q9ULH0				Q9ULH0			
ID	Q9ULH0	PRELIMINARY;	PRT; 1777 AA.	ID	Q9ULH0	PRELIMINARY;	PRT; 1777 AA.	ID	Q9ULH0	PRELIMINARY;	PRT; 1777 AA.

Db	1108	DKGKFTPLILAAATAGHVGVVEILLDNGADIEAQSERTKDTPSLACSGGROEVELLAR	1167
QY	180	DVD--INYYDWNGGTPLLYAVRGNHVKCVEALLARGADLTTEADS--GYTPMDLAVALG	234
Db	1168	GANKEHNRVSDY---TPLSLAAASGGYVNIKILLNAGAEINSRTGSKLGISPLMLAAMNG	1224

Search completed: March 17, 2003, 16:40:42
Job time : 39 secs

